

Figure 1. 158P1D7 SSH sequence (SEQ ID NO:655).

```
1 GATCTGATAA GCTTTCAATG TTGCGCTCCT GACAATGTAT TAGAAGTCCT GATGGGGATA
61 GGACTTTGCA GTTACAAGGA ATAGGGCAGA AAGGTCCTGG AAGTTGAGTG GATGGCTTTG
121 TAATATAAGG TATCAAACCT GGTGCTTTGG TGGGTAGTTT TAGAATGGAC GTGGTCTTAG
181 TTGACATGCG ACTATCATTT ATTGAAGATG TTGCTGCCAG ATGTAATGAT C
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Figure 2. 158P1D7 cDNA clone TurboScript3PX and open reading frame (ORF)

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1           M K L W I H L F Y S S L L
1 t c g g a t t t c a t c a c a t g a c a a c a t g a a g c t g t g g a t t c a t c t c t t t t a t t c a t c t c t c c t
14 A C I S L H S Q T P V L S S R G S C D S
61 T G C C T G T A T A T C T T T A C A C T C C C A A A C T C C A G T G C T C T C A T C C A G A G G C T C T T G T G A T T C
34 L C N C E E K D G T M L I N C E A K G I
121 T C T T T G C A A T T G T G A G G A A A A G A T G G C A C A A T G C T A A T A A A T T G T G A A G C A A A A G G T A T
54 K M V S E I S V P P S R P F Q L S L L N
181 C A A G A T G G T A T C T G A A A T A A G T G T G C C A C C A T C A C G A C T T T C C A A C T A A G C T T A T T A A A
74 N G L T M L H T N D F S G L T N A I S I
241 T A A C G G C T T G A C G A T G C T T C A C A C A A A T G A C T T T T C T G G G C T T A C C A A T G C T A T T T C A A T
94 H L G F N N I A D I E I G A F N G L G L
301 A C A C C T T G G A T T T A A C A A T A T T G C A G A T A T T G A G A T A G G T G C A T T T A A T G G C C T T G G C C T
114 L K Q L H I N H N S L E I L K E D T F H
361 C C T G A A A C A A C T T C A T A T C A A T C A C A A T T C T T T A G A A A T T C T T A A G A G G A T A C T T T C C A
134 G L E N L E F L Q A D N N F I T V I E P
421 T G G A C T G G A A A A C C T G G A A T T C C T G C A A G C A G A T A A C A A T T T T A T C A C A G T G A T T G A A C C
154 S A F S K L N R L K V L I L N D N A I E
481 A A G T G C C T T T A G C A A G C T C A A C A G A C T C A A A G T G T T A A T T T T A A T G A C A A T G C T A T T G A
174 S L P P N I F R F V P L T H L D L R G N
541 G A G T C T T C C T C C A A C A T C T T C C G A T T T T C C T T T A A C C C A T C T A G A T C T T C G T G G A A A
194 Q L Q T L P Y V G F L E H I G R I L D L
601 T C A A T T A C A A A C A A T T G C C T T A T G T T G G T T T T C T C G A A C A C A T T G G C C G A A T A T T G G A T C T
214 Q L E D N K W A C N C D L L Q L K T W L
661 T C A G T T G G A G G A C A A C A A A T G G G C C T G C A A T T G T G A C T T A T T G C A G T T A A A A C T T G G T T
234 E N M P P Q S I I G D V V C N S P P F F
721 G G A G A A C A T G C C T C C A C A G T C T A T A A T T G G T G A T G T T G T C T G C A A C A G C C C T C C A T T T T T
254 K G S I L S R L K K E S I C P T P P V Y
781 T A A G G A A G T A T A C T C A G T A G A C T A A A G A A G G A A T C T A T T T G C C C T A C T C C A C C A G T G T A
274 E E H E D P S G S L H L A A T S S I N D
841 T G A A G A A C A T G A G G A T C C T T C A G G A T C A T T A C A T C T G G C A G C A A C A T C T T C A A T A A A T G A
294 S R M S T K T T S I L K L P T K A P G L
901 T A G T C G C A T G T C A A C T A A G A C C A C G T C C A T T C T A A A A C T A C C C A C C A A G C A C C A G G T T T
314 I P Y I T K P S T Q L P G P Y C P I P C
961 G A T A C C T T A T A T T A C A A A G C C A T C C A C T C A A C T T C C A G G A C C T T A C T G C C C T A T T C C T T G
334 N C K V L S P S G L L I H C Q E R N I E
1021 T A A C T G C A A A G C C T A T C C C C A T C G A C T T C T A A T A C A T T G T C A G G A G C G C A A C A T T G A
354 S L S D L R P P P Q N P R K L I L A G N
1081 A A G C T T A T C A G A T C T G A G A C C T C C T C C G C A A A A T C C T A G A A A G C T A T T C T A G C G G G A A A
374 I I H S L M K S D L V E Y F T L E M L H
1141 T A T T A T T C A C A G T T T A A T G A A G T C T G A T C T A G T G G A A T A T T T C A C T T T G G A A A T G C T T C A
394 L G N N R I E V L E E G S F M N L T R L
1201 C T T G G G A A A C A A T C G T A T T G A A G T T C T T G A A G A A G G A T C G T T T A T G A A C C T A A C G A G A T T
414 Q K L Y L N G N H L T K L S K G M F L G
1261 A C A A A A A C T C T A T C T A A A T G G T A A C C A C C T G A C C A A A T T A A G T A A A G G C A T G T T C C T T G G
434 L H N L E Y L Y L E Y N A I K E I L P G
1321 T C T C C A T A A T C T T G A A T A C T T A T A T C T T G A A T A C A A T G C C A T T A A G G A A A T A C T G C C A G G
454 T F N P M P K L K V L Y L N N N L L Q V
1381 A A C C T T T A A T C C A A T G C C T A A A C T T A A A G T C C T G T A T T T A A A T A A C A A C C T C C T C C A A G T
474 L P P H I F S G V P L T K V N L K T N Q
1441 T T T A C C A C C A C A T A T T T T T C A G G G G T T C C T C T A A C T A A G G T A A A T C T T A A A C A A A C C A
494 F T H L P V S N I L D D L D L L T Q I D
1501 G T T T A C C C A T C T A C C T G T A A G T A A T A T T T T G G A T G A T C T T G A T T T A C T A A C C C A G A T T G A
514 L E D N P W D C S C D L V G L Q Q W I Q

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1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA
534 K L S K N T V T D D I L C T S P G H L D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCGGGCATCTCGA
554 K K E L K A L N S E I L C P G L V N N P
1681 CAAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
574 S M P T Q T S Y L M V T T P A T T N T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAAATAC
594 A D T I L R S L T D A V P L S V L I L G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
614 L L I M F I T I V F C A A G I V V L V L
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTC
634 H R R R R Y K K K Q V D E Q M R D N S P
1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
654 V H L Q Y S M Y G H K T T H H T T E R P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACTACTGAAAGACC
674 S A S L Y E Q H M V S P M V H V Y R S P
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC
694 S F G P K H L E E E E E R N E K E G S D
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA
714 A K H L Q R S L L E Q E N H S P L T G S
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGAACAGGAAAATCATTCACTCAGGGTCT
734 N M K Y K T T N Q S T E F L S F Q D A S
2221 AAATATGAAATACAAAACCACGAACCAATCAACAGAATTTTATCCTTCCAAGATGCCAG
754 S L Y R N I L E K E R E L Q Q L G I T E
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAACCTCAGCAACTGGGAATCACAGA
774 Y L R K N I A Q L Q P D M E A H Y P G A
2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC
794 H E E L K L M E T L M Y S R P R K V L V
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT
814 E Q T K N E Y F E L K A N L H A E P D Y
2461 GGAACAGACAAAAAATGAGTATTTTGAACCTAAAGCTAATTTACATGCTGAACCTGACTA
834 L E V L E Q Q T * (SEQ ID NO:657)
2521 TTTAGAAGTCCTGGAGCAGCAAACATAGatggaga (SEQ ID NO:656)

Figure 3. 158P1D7 amino acid sequence.

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1 MKLWIHLFYS SLLACISLHS QTPVLSSRGs CDSLNCNEEK DGTMLINCEA KGIKMVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDfSGLTNA ISIHlGFNNI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENLEF LQADNNFITV IEPsAFsKLN RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTLpY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGsFMNL TRlQKLyLNG
421 NHLTKLSKGM FLGLHNLEYL YLEYNAlKEI LPGTfNPMPK LKVLYLNNNL LQVLPPHIFS
481 GVPLTKVNLK TNQfTHLPVS NILDdLLdLLT QIDLEDNPWD CSCDLVGLQQ WlQKLsKNTV
541 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVtTPATT TNTADtILRS
601 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM
661 YGHKTTHHTT ERPSASLYEQ HMVSPMVHVY RSPsFGPKHL EEEEEERNEKE GSDAKHLQRS
721 LLEQENHSPL TGsNMKYKTT NQSTEFsFSQ DASSLYRNIL EKERELeQLG ITeYLrKNIA
781 QLQPDMEAHY PGaHEELKLM ETLMySRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ
841 T* (SEQ ID NO:657)
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158P1D7

Figure 4. 158PID7 amino acid BLAST homology to hypothetical protein FLJ27774.

Identities = 798/798 (100%)

Query: 44 MLINCEAKGIKVMSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIH LGFNNIADI 103
 MLINCEAKGIKVMSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIH LGFNNIADI
 Sbjct: 1 MLINCEAKGIKVMSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIH LGFNNIADI 60

Query: 104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENL EFLQADNNFITVIEPSAFSKLNRLK 163
 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENL EFLQADNNFITVIEPSAFSKLNRLK
 Sbjct: 61 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENL EFLQADNNFITVIEPSAFSKLNRLK 120

Query: 164 VLILNDNAIESLPPNIFRFVPLTHLDRGNQLQTL PYVGFLEHIGRILDQLQLEDNKWACN 223
 VLILNDNAIESLPPNIFRFVPLTHLDRGNQLQTL PYVGFLEHIGRILDQLQLEDNKWACN
 Sbjct: 121 VLILNDNAIESLPPNIFRFVPLTHLDRGNQLQTL PYVGFLEHIGRILDQLQLEDNKWACN 180

Query: 224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSIL SRLKKESICPTPPVYEEHEDPSGSL 283
 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSIL SRLKKESICPTPPVYEEHEDPSGSL
 Sbjct: 181 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSIL SRLKKESICPTPPVYEEHEDPSGSL 240

Query: 284 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYIT KPSTQLPGPYCPIPCNCKVLSPSGL 343
 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYIT KPSTQLPGPYCPIPCNCKVLSPSGL
 Sbjct: 241 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYIT KPSTQLPGPYCPIPCNCKVLSPSGL 300

Query: 344 LIHCQERNIESLSDLRPPQNPRLKILAGNIIHSL MKSDLVEYFTLEMLHLGNNRIEVL 403
 LIHCQERNIESLSDLRPPQNPRLKILAGNIIHSL MKSDLVEYFTLEMLHLGNNRIEVL
 Sbjct: 301 LIHCQERNIESLSDLRPPQNPRLKILAGNIIHSL MKSDLVEYFTLEMLHLGNNRIEVL 360

Query: 404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHN LEYLYLEYNAIKEILPGTFNMPMKLV 463
 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHN LEYLYLEYNAIKEILPGTFNMPMKLV
 Sbjct: 361 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHN LEYLYLEYNAIKEILPGTFNMPMKLV 420

Query: 464 LYLNNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLP VSNILDDDLLTQIDLEDNPWD CSC 523
 LYLNNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLP VSNILDDDLLTQIDLEDNPWD CSC
 Sbjct: 421 LYLNNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLP VSNILDDDLLTQIDLEDNPWD CSC 480

Query: 524 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKE LKALNSEILCPGLVNNPSMPTQTSYLM 583
 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKE LKALNSEILCPGLVNNPSMPTQTSYLM
 Sbjct: 481 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKE LKALNSEILCPGLVNNPSMPTQTSYLM 540

Query: 584 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMF ITIVFCAAGIVVLVLRHRRRYKKKQ 643
 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMF ITIVFCAAGIVVLVLRHRRRYKKKQ
 Sbjct: 541 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMF ITIVFCAAGIVVLVLRHRRRYKKKQ 600

Query: 644 VDEQMRDN SPVHLQYS MYGHKTTHHTTERPSAS LYEQHMVSPMVHVYRSPSFGPKHLEEE 703
 VDEQMRDN SPVHLQYS MYGHKTTHHTTERPSAS LYEQHMVSPMVHVYRSPSFGPKHLEEE
 Sbjct: 601 VDEQMRDN SPVHLQYS MYGHKTTHHTTERPSAS LYEQHMVSPMVHVYRSPSFGPKHLEEE 660

Query: 704 EERNEKEGSDAKHLQRSLL EQENHSPLTGSNMKY KTTNQSTEFLSFQDASSLYRNILEKE 763
 EERNEKEGSDAKHLQRSLL EQENHSPLTGSNMKY KTTNQSTEFLSFQDASSLYRNILEKE
 Sbjct: 661 EERNEKEGSDAKHLQRSLL EQENHSPLTGSNMKY KTTNQSTEFLSFQDASSLYRNILEKE 720

Query: 764 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEEL KLMETLMYSRPRKVLVEQTKNEYFEL 823
 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEEL KLMETLMYSRPRKVLVEQTKNEYFEL
 Sbjct: 721 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEEL KLMETLMYSRPRKVLVEQTKNEYFEL 780

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
OTHER CANCERS

First Inventor: Mary FARIS, et al.

Application No.: To be assigned

Docket No.: 51158-20050.00

Sheet 6 of 20

Query: 824 KANLHAEPDYLEVLEQQT 841
KANLHAEPDYLEVLEQQT

Sbjct: 781 KANLHAEPDYLEVLEQQT 798 (SEQ ID NO:658)

sd-53617

Figure 5a: Alignment of 158P1D7 with human FLJ22774, CLONE KAIA1575. [Homo sapiens]

Identities = 405/415 (97%), Positives = 405/415 (97%)

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158P1D7: 44 MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
              MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI
Sbjct: 1      MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

158P1D7:104 EIGAFNGLGLLKQLHINHNLSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK 163
              EIGAFNGLGLLKQLHINHNLSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61     EIGAFNGLGLLKQLHINHNLSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK 120

158P1D7:164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLHEHIGRILDLQLEDNKWACN 223
              VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLHEHIGRILDLQLEDNKWACN
Sbjct: 121    VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLHEHIGRILDLQLEDNKWACN 180

158P1D7:224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKEICPTPPVYEEHEDPSGSL 283
              CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKEICPTPPVYEEHEDPSGSL
Sbjct: 181    CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKEICPTPPVYEEHEDPSGSL 240

158P1D7:284 HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
              HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241    HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

158P1D7:344 LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDDLVEYFTLEMLHLGNRNRIEVL 403
              LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDDLVEYFTLEMLHLGNRNRIEVL
Sbjct: 301    LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDDLVEYFTLEMLHLGNRNRIEVL 360

158P1D7:404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNPM 458
              EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLH AIKEILPGTFNPM
Sbjct: 361    EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLLEYLYLEYNAIKEILPGTFNPM 415 (SEQ ID
NO:659)

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Figure 5b: Alignment of 158P1D7 protein with a human protein similar to IGFALS

Identities = 316/864 (36%), Positives = 459/864 (52%)

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158P1D7:1  MKLWIHLFYSSLLACISLSHSQTPVLSSRGSCDSLNCCEKDGTM LINCEAKGIKMVSEIS 60
              M LW+ L S+L++ + S V ++C+C + + +NCE + +++
Sbjct: 17   MFLWLFLILSALISSTNADSDISV-----EICNVCSCVSVENVLYVNCEKVSRYRPNQLK 71

158P1D7:61  VPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI EIGAFNGLGLLKQLHIN 120
              P S + L+ NN L +L+ N F ++A+S+HLG N + +IE GAF GL LKQLH+N
Sbjct: 72   PPWSNFYHLNFQNNFLNILYPNTFLNFSHAVSLHLGNKQLQNI EGGAFLGLSALKQLHLN 131

158P1D7:121 HNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESLPPNIF 180
              +N L+IL+ DTF G+ENLE+LQAD N I IE AF+KL++LKVLI LNDN I LP NIF
Sbjct: 132  NNELKILRADTFGLIENLEYLQADYNLIK YIERGAFNKLHKLKVLI LNDNLISFLPDNIF 191

158P1D7:181 RFVPLTHLDLRGNQLQTLPHYVGFLHEHIGRILDLQLEDNKWACNCDLLQLKTWLENMPPQS 240
              RF LTHLD+RGN++Q LPY+G LEHIGR+++LQLEDN W C+CDLL LK WLENMP
Sbjct: 192  RFASLTHLDIRGNRIQKLPYIGVLEHIGRVVELQLEDNPWNCSDDLPLKAWLENMPYNI 251

158P1D7:241 IIGDVVCNSPPFFKGSILSRLKKEICP-----TPPVYEEHEDPSGSLHLAATS 289
              IG+ +C +P G +L K+ +CP PP E+ + + H TS
Sbjct: 252  YIGEAICTPSDLYGRLLKETNKQELCPMGTSDFDVRILPPSQLENGYTTPNGHTTQTS 311

158P1D7:290 SINDSRMSTKTTSSILKLPTKAPGLI-----PYITKPSTQLPG-PYCPIPCNCKV- 337
              KTT+ P+K G++ I T++P CP PC CK
Sbjct: 312  LHRLVTKPPKTTN----PSKISGIVAGKALSNRNLSQIVSYQTRVPPLTPCPAPCFCKTH 367

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158P1D7:338 LSPSGLLIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKS DLVEYFTLEMLHLGNN 397
S GL ++CQE+NI+S+S+L P P N +KL + GN I + SD ++ L++LHLG+N
Sbjct: 368 PSDLGLSVNCQEKNIQSMSELIPKPLNAKLVNGNSIKD VDVSDFTDFEGLDLLHLGNN 427

158P1D7:398 RIEVLEEGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNP 457
+I V++ F NLT L++LYLNGN + +L +F GLH IKEI GTF+
Sbjct: 428 QITVIKGDVFNLTNLRLRLYLNNGNQLERLYPEIFSGLHNLQYLYLEYNLIKEISAGTFDS 487

158P1D7:458 MXXXXXXXXXXXXXXXXXHFSGVPLTKVNLKTNQFTHLPVSNIXXXXXXXXXXXXXXXXXN 517
M +IFSG PL ++NL+ N+F +LPVS + N
Sbjct: 488 MPNLQLLYLNNLLKSLPVYIFSGAPLARLNLNRNNKFMYPVSGVLDQLQSLTQIDLEGN 547

158P1D7:518 PWDCSCDLVGLQQWIKLSKNTVTDDILCTSPGHLDDKELKALNSEILCPGLVNNPSMPT 577
PWDC+CDLV L+ W++KLS V ++ C +P ELK+L +EILCP L+N PS P
Sbjct: 548 PWDCTCDLVALKLWVEKLSDGIVVKELKCTPVQFANIELKSLKNEILCPKLLNKPSAP- 606

158P1D7:578 QTSYLMVXXXXXXXXXXXXXILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVLRHR 637
+ I VPLS+LIL +L++ I VF A ++V VL R +
Sbjct: 607 ---FTSPAPAITFTTPLGPIRSPPGPVPLSILILSVLVLILTVFVAFCLLVFVLRNRK 663

158P1D7:638 RYKKKQVDEQMRDNPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGP 697
+ K D + LQ + HK T + E + + +S + G
Sbjct: 664 KPTVKHEGLGNPDCGSMQLQLRKHDHK-----TNKKDGLSTEAFIPQTIEQMSKSHTCGL 718

158P1D7:698 KHLXXXXXXXXXXGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYR 757
K G K + R++ ++E + + T ++ E +D++ +
Sbjct: 719 KESETGFMFSDPPGQ--KVMRNVADKEKDLLHVDTRKRLSTIDELDELFPSSRDSNVFIQ 776

158P1D7:758 NILEKERELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTK 817
N LE ++E +G++ + E YP + K ++L+ K++VEQ K
Sbjct: 777 NFLESKKEYNSIGVSGF-----EIRYPEKQPDKSKKSLIGGNHISKIVVEQRK 824

158P1D7:818 NEYFELKANLHAEPDYLEVLEQQT 841
+EYFELKA L + PDYL+VLE+QT
Sbjct: 825 SEYFELKAKLQSSPDYLQVLEEQT 848 (SEQ ID NO:660)

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
OTHER CANCERS
First Inventor: Mary FARIS, et al.
Application No.: To be assigned
Docket No.: 51158-20050.00
Sheet 8 of 20

Figure 6. Expression of 158P1D7 by RT-PCR

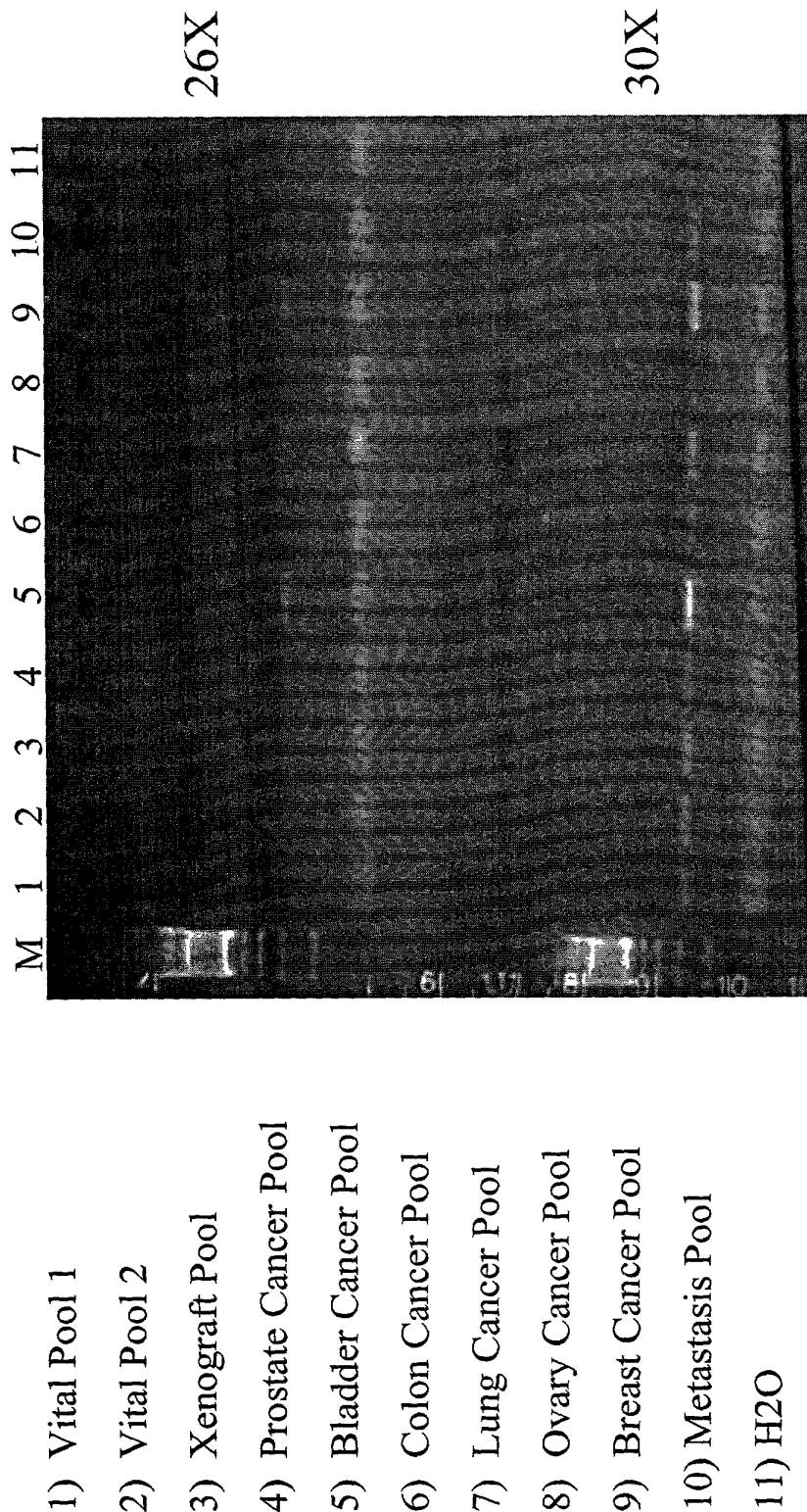


Figure 7. Expression of 158P1D7 in Normal Tissues

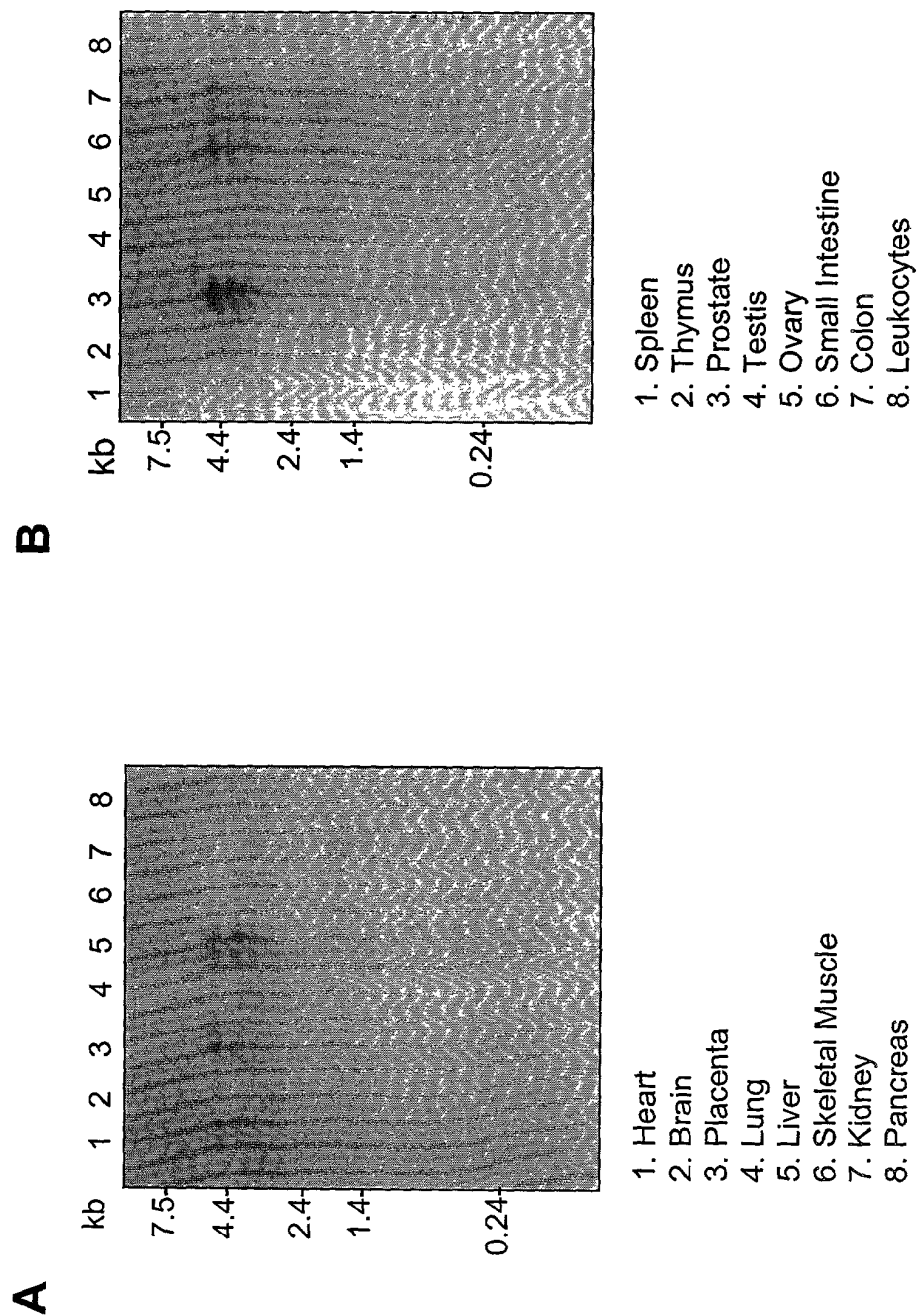
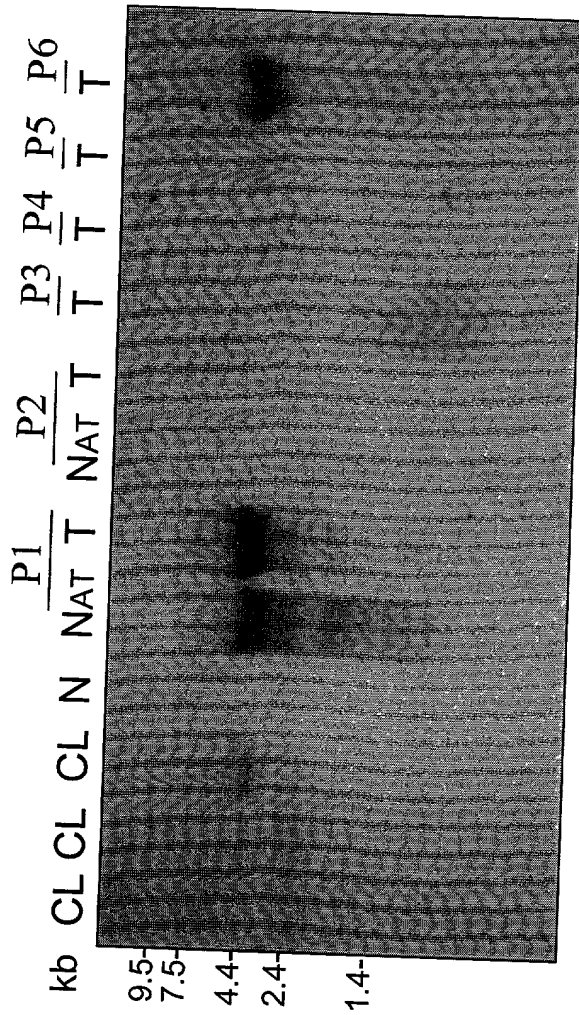


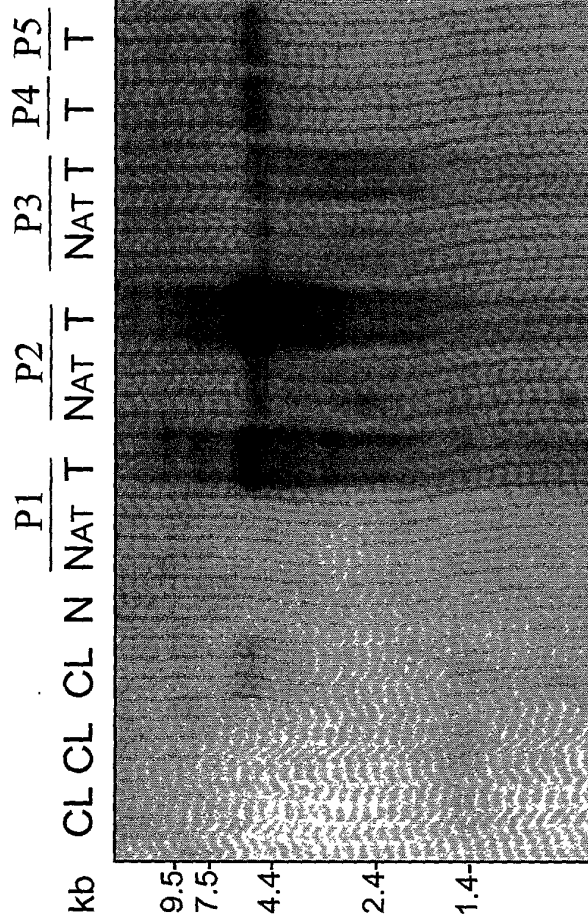
Figure 8A. Expression of 158P1D7 in Bladder Cancer Patient Specimens



P1 - Transitional, grade 4
P2 - Squamous inv.
P3 - Transitional, grade 3
P4 - Papillary non-inv, grade 1/3
P5 - Papillary, grade 3/3
P6 - Transitional, grade 3/2

CL = Cell lines (listed in order): UM-UC-3, J82, SCaBER
P = Patient
N = Normal Bladder
NAT = Normal adjacent tissue
T = Tumor

Figure 8B. Expression of 158P1D7 in Bladder Cancer Patient Specimens



P1 - Transitional, grade 2
P2 - Transitional, grade 3/2
P3 - Transitional,
P4 - Polypoid Cystitis
P5 - Papillary, grade 3/3

CL = Cell lines (from left to right):
UM-UC-3, J82, SCaBER
P = Patient
N = Normal Bladder
NAT = Normal adjacent tissue
T = Tumor

Figure 9. Expression of 158P1D7 in Lung Cancer Patient Specimens

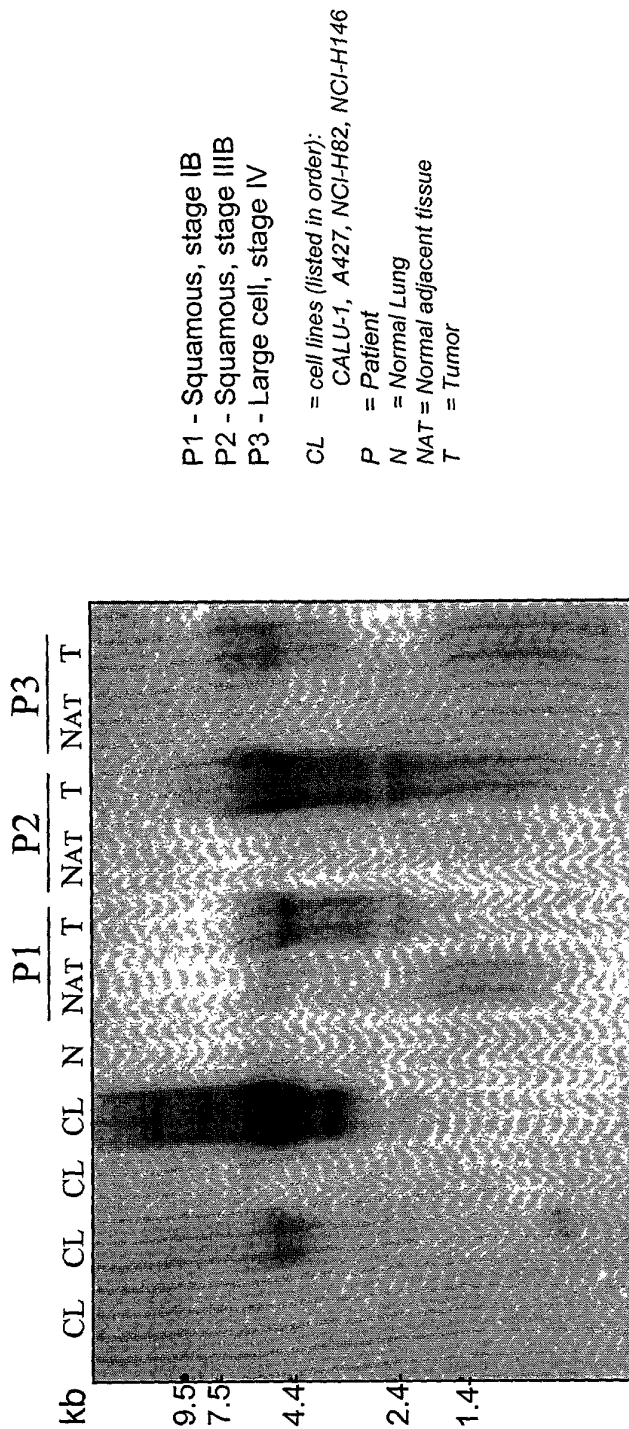


Figure 10. Expression of 158P1D7 in Breast Cancer Patient Specimens

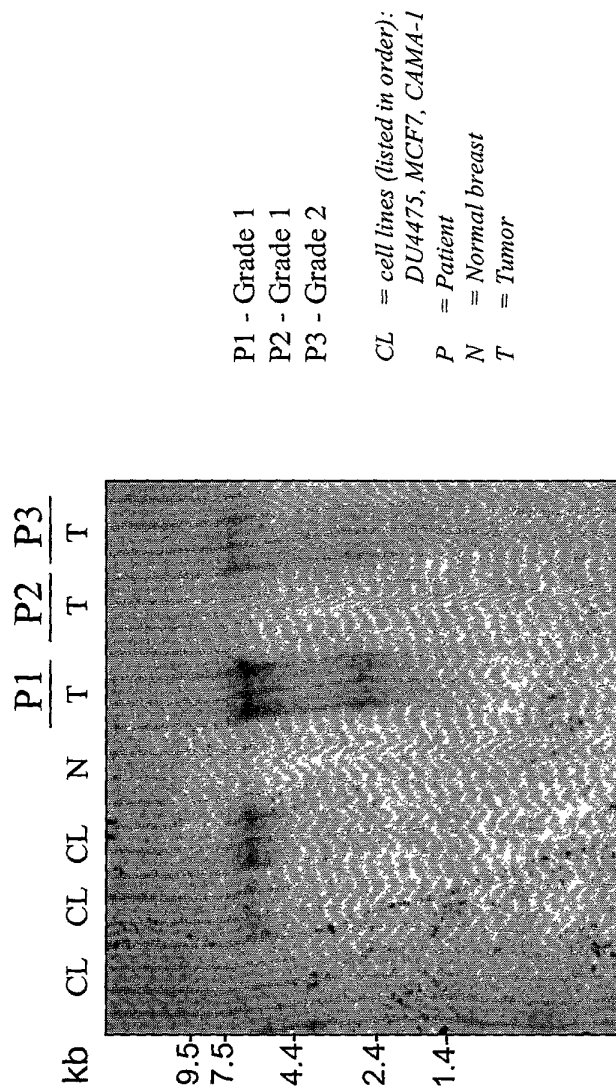


Figure 11. 158P1D7 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

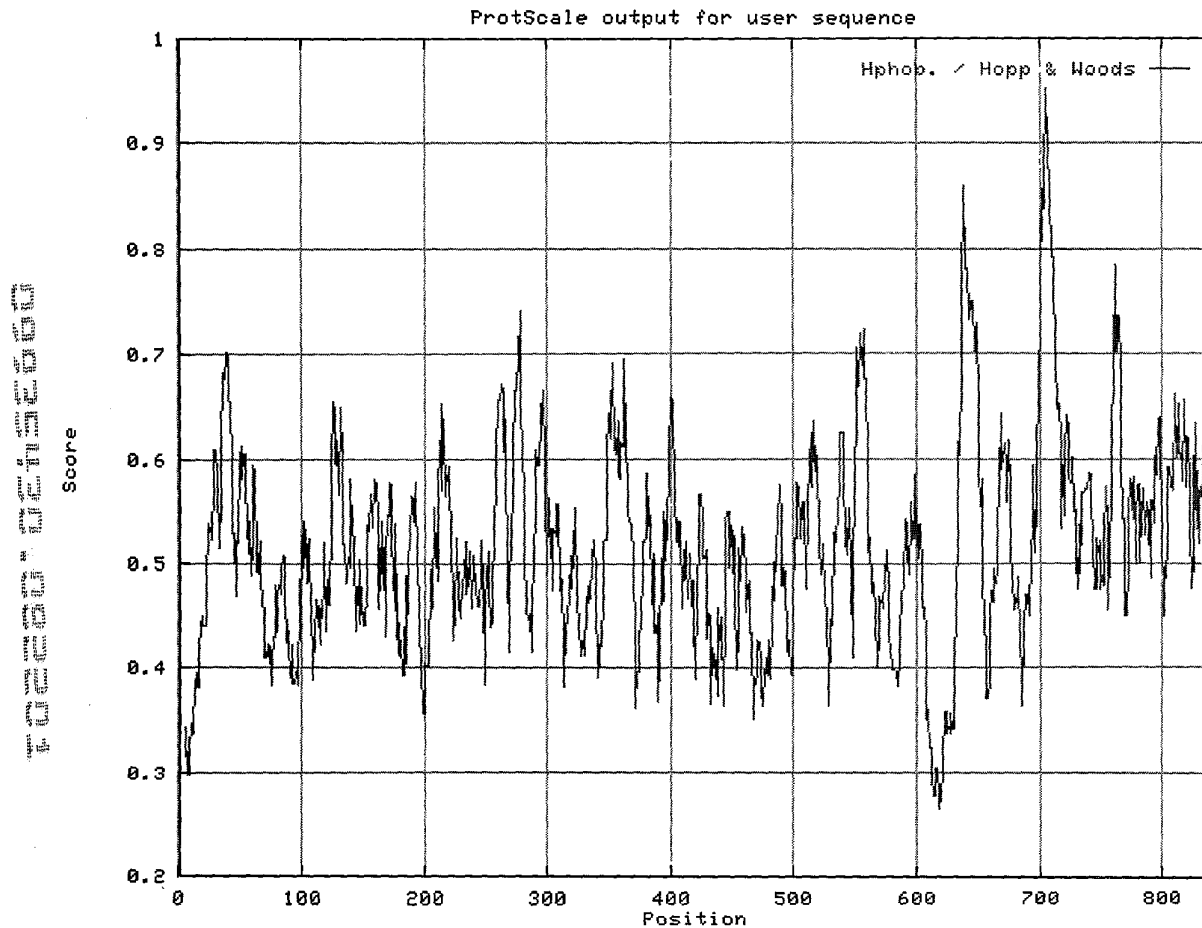


Figure 12. 158P1D7 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

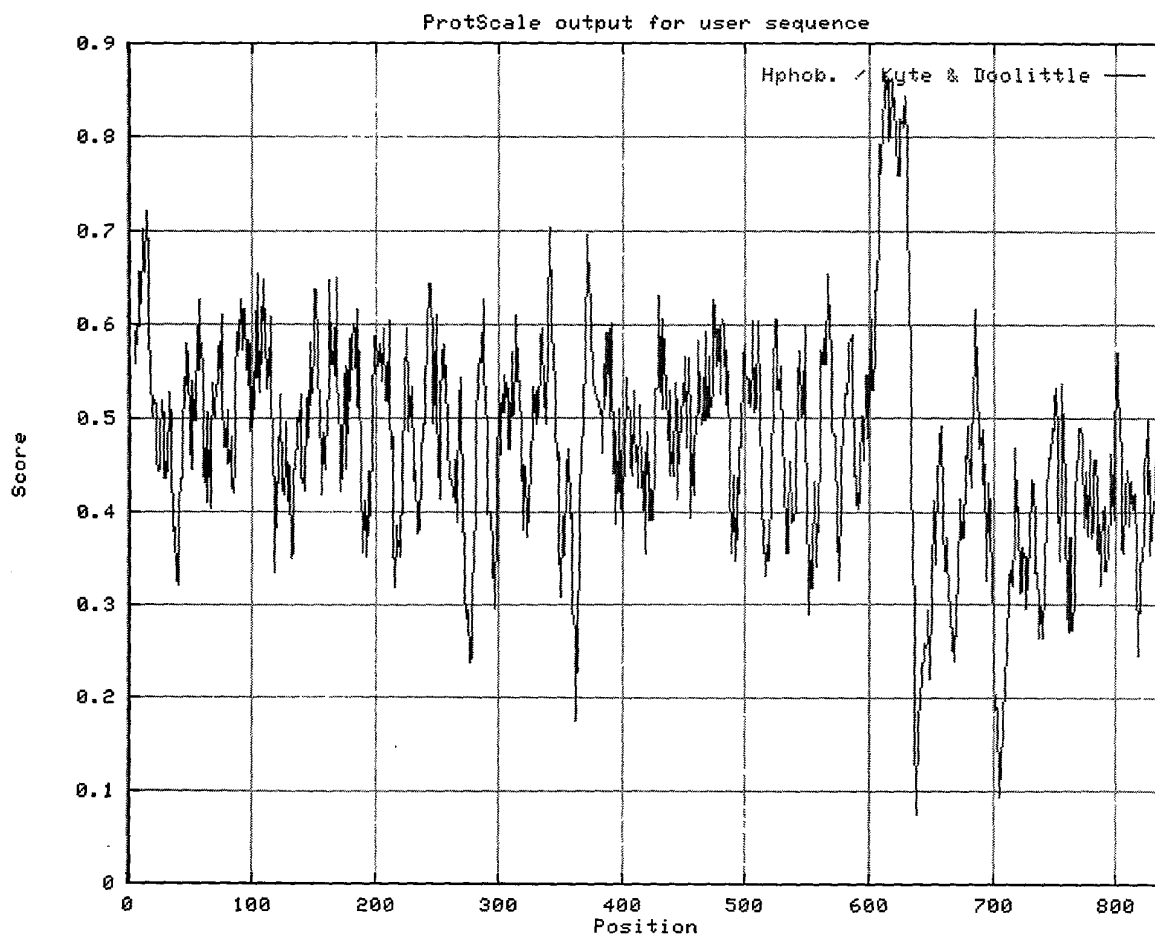


Figure 13. 158P1D7 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

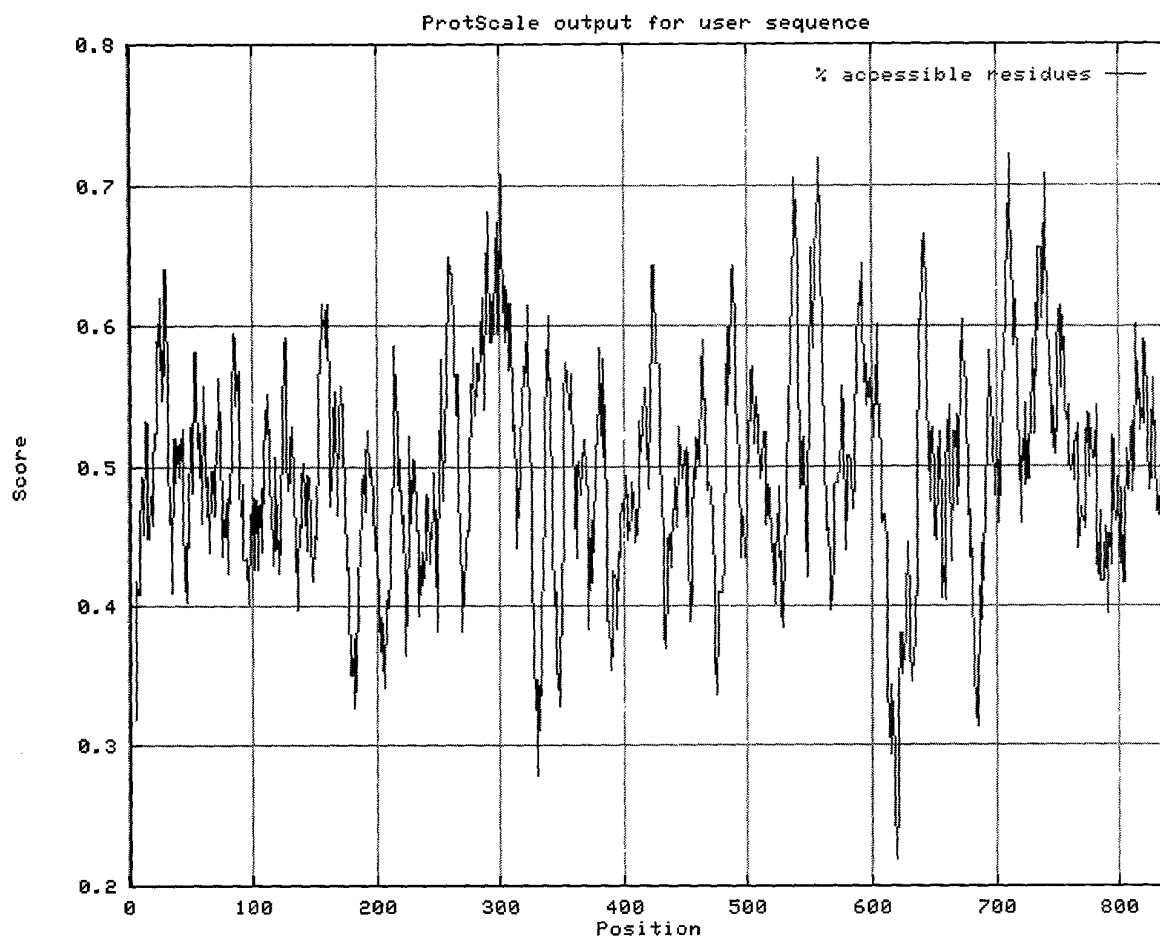


Figure 14. 158P1D7 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

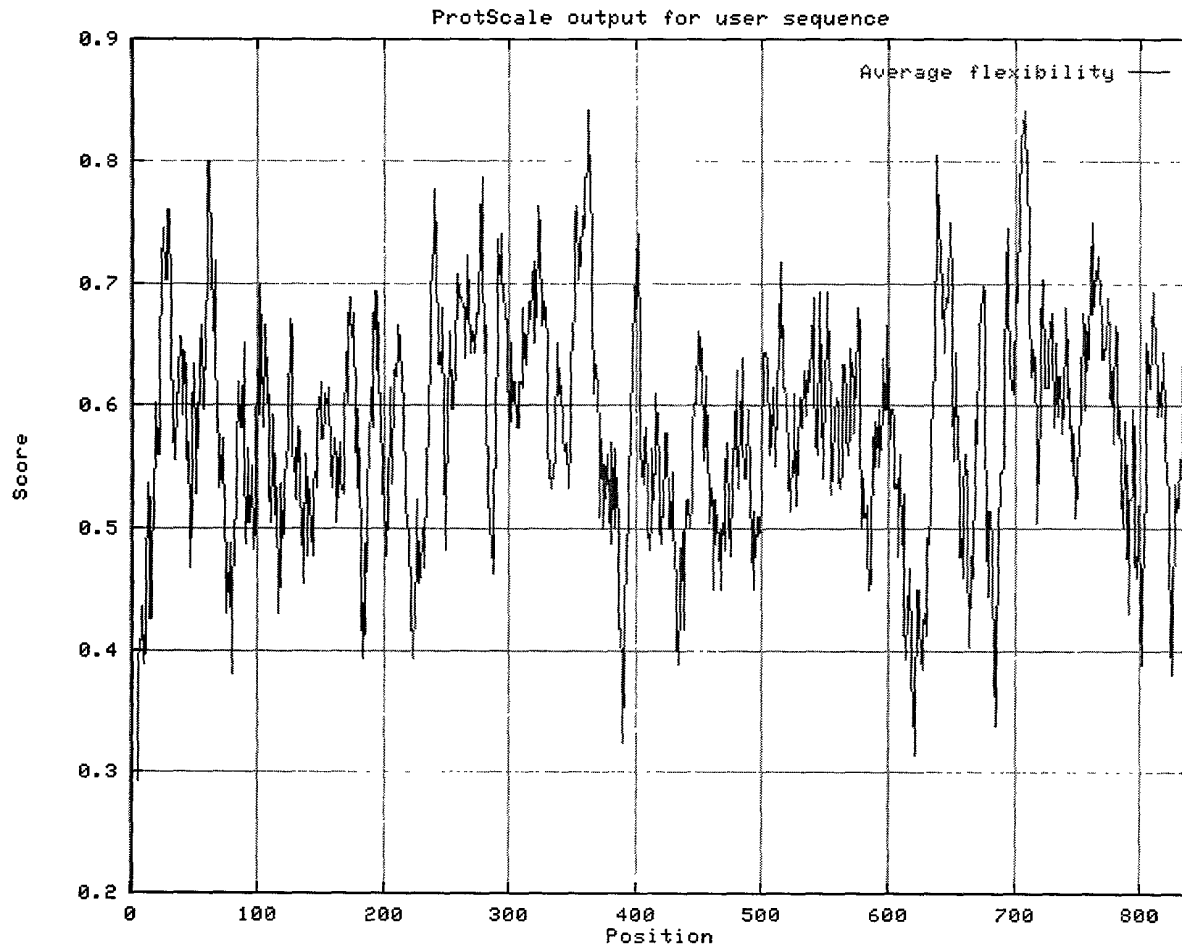


Figure 15. 158P1D7 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

